

Sphingomonas ORF1

ATG ACC GAT CCA CGT CAG CTG CAC CTG GCC GGA TTC TTC TGT GCC GGC AAC GTC ACG CAC 60
 Met Thr Asp Pro Arg Gln Leu His Leu Ala Gly Phe Phe Cys Ala Gly Asn Val Thr His
 1 5 10 15 20
 GCC CAC GGA GCG TGG CGC CAC GGC GAC TCC AAC GGC TTC CTC ACC AAG GAG TAC TAC 120
 Ala His Gly Ala Trp Arg His Ala Asp Asp Ser Asn Gly Phe Leu Thr Lys Glu Tyr Tyr
 25 30 35 40
 CAG CAG ATT GCC CGC ACG CTC GAG CGC GGC AAG TTC GAC CTG CTG TTC CTT CCC GAC GCG 180
 Gln Gln Ile Ala Arg Thr Leu Glu Arg Gly Lys Phe Asp Leu Leu Phe Leu Pro Asp Ala
 45 50 55 60
 CTC GCC GTG TGG GAC AGC TAC GGC GAC AAT CTG GAG ACC GGT CTG CGG TAT GGC GGC CAA 240
 Leu Ala Val Trp Asp Ser Tyr Gly Asp Asn Leu Glu Thr Gly Leu Arg Tyr Gly Gln
 65 70 75 80
 GGC GCG GTG ATG CTG GAG CCC GGC GTA GTT ATC GCC GCG ATG GCC TCG GTG ACC GAA CAT 300
 Gly Ala Val Met Leu Glu Pro Gly Val Val Ile Ala Ala Met Ala Ser Val Thr Glu His
 85 90 95 100
 CTG GGC CTG GGC ACC ATT TCC ACC ACC TAC TAC CCG CCC TAC CAT GTA GCC CGG GTC 360
 Leu Gly Leu Gly Ala Thr Ile Ser Thr Thr Thr Tyr Tyr Pro Pro Tyr His Val Ala Arg Val
 105 110 115 120
 GTC GCT TCG CTG GAC CAG CTG TCC TCC GGC CGA GTG TCG TGG AAC GTG GTC ACC TCG CTC 420
 Val Ala Ser Leu Asp Gln Leu Ser Ser Gly Arg Val Ser Trp Asn Val Val Thr Ser Leu
 125 130 135 140

FIG. 1A

Sphingomonas ORF1 (cont.)

AGC AAT GCA GAG GCG CGC AAC TTC GGC TTC GAT GAA CAT CTC GAC CAC GAT GCC CGC TAC	480
Ser Asn Ala Glu Ala Arg Asn Phe Gly Phe Asp Glu His Leu Asp His Asp Ala Arg Tyr	150
145	155
GAT CGC GCC GAT GAA TTC CTC GAG GTC GTG CGC AAG CTC TGG AAC AGC TGG GAT CGC GAT	540
Asp Arg Ala Asp Glu Phe Leu Glu Val Val Arg Lys Leu Trp Asn Ser Trp Asp Arg Asp	170
165	175
GCG CTG ACA CTC GAC AAG GCA ACC GGC CAG TTC GCC GAT CCG GCT AAG GTG CGC TAC ATC	600
Ala Leu Thr Leu Asp Lys Ala Thr Gly Gln Phe Ala Asp Pro Ala Lys Val Arg Tyr Ile	190
185	195
GAC CAC CGC GGC GAA TGG CTC AAC GTA CGC GGG CCG CTT CAG GTG CCG CGC TCC CCC CAG	660
Asp His Arg Gly Glu Trp Leu Asn Val Arg Gly Pro Leu Gln Val Pro Arg Ser Pro Gln	210
205	215
GGC GAG CCT GTC ATT CTG CAG GCC GGC GGT TCG GCG CGG GGC AAG CGC TTC GCC GGC CGC	720
Gly Glu Pro Val Ile Leu Gln Ala Gly Leu Ser Ala Arg Gly Lys Arg Phe Ala Gly Arg	230
225	235
TGG GCG GAC GCG GTG TTC ACG ATT TCG CCC AAT CTG GAC ATC ATG CAG GCC ACG TAC CGC	780
Trp Ala Asp Ala Val Phe Thr Ile Ser Pro Asn Leu Asp Ile Met Gln Ala Thr Tyr Arg	250
245	255
GAC ATA AAG GCG CAG GTC GAG GCC GCC GGA CGC GAT CCC GAG CAG GTC AAG GTG TTT GCC	840
Asp Ile Lys Ala Gln Val Glu Ala Ala Gly Arg Asp Pro Glu Gln Val Lys Val Phe Ala	270
265	275

FIG. 1B

Sphingomonas ORF1 (cont)

GCG GTG ATG CCG ATC CTC GGC GAG ACC GAG GCG ATC GCC AGG CAG CGT CTC GAA TAC ATA	900
Ala Val Met Pro Ile Leu Gly Glu Thr Glu Ala Ile Ala Arg Gln Arg Leu Glu Tyr Ile	300
285	290
AAT TCG CTG GTG CAT CCC GAA GTC GGG CTT TCT ACC TTG TCC AGC CAT GTC GGG GTC AAC	960
Asn Ser Leu Val His Pro Glu Val Gly Leu Ser Thr Leu Ser Ser His Val Gly Val Asn	320
305	310
CTT GCC GAC TAT TCG CTC GAT ACC CCG CTG ACC GAG GTC GGC GAT CTC GCC CAG CGC	1020
Leu Ala Asp Tyr Ser Leu Asp Thr Pro Leu Thr Glu Val Leu Gly Asp Leu Ala Gln Arg	340
325	330
AAC GTG CCC ACC CAA CTG GGC ATG TTC GCC AGG ATG TTG CAG GCC GAG ACC CTG ACC GTG	1080
Asn Val Pro Thr Gln Leu Gly Met Phe Ala Arg Met Leu Gln Ala Glu Thr Leu Thr Val	360
345	350
GGA GAA ATG GGC CGG CGT TAT GGC GCC AAC GTG GGC TTC GTC CCG CAG TGG GCG GGA ACC	1140
Gly Glu Met Gly Arg Arg Tyr Gly Ala Asn Val Gly Phe Val Pro Gln Trp Ala Gly Thr	380
365	370
CGC GAG CAG ATC GCG GAC CTG ATC GAG ATC CAT TTC AAG GCC GGC GGC GAT GGC TTC	1200
Arg Glu Gln Ile Ala Asp Leu Ile Glu Ile His Phe Lys Ala Gly Ala Asp Gly Phe	400
385	390
ATC ATC TCG CCG GCG TTC CTG CCC GGA TCT TAC GAG GAA TTC GTC GAT CAG GTG GTG CCC	1260
Ile Ile Ser Pro Ala Phe Leu Pro Gly Ser Tyr Glu Glu Phe Val Asp Gln Val Val Pro	420
405	410

FIG. 1C

Sphingomonas ORF1 (cont)

1320

ATC CTG CAG CAC CGC GGA CTG TTC CGC ACT GAT TAC GAA GGC CGC ACC CTG CGC AGC CAT
 Ile Leu Gln His Arg Gly Leu Phe Arg Thr Asp Tyr Glu Gly Arg Thr Leu Arg Ser His
 425 430 435 440

CTG GGA CTG CGT GAA CCC GCA TAC CTG GGA GAG TAC GCA TGA
 Leu Gly Leu Arg Glu Pro Ala Tyr Leu Gly Glu Tyr Ala
 445 450

FIG. 1D

Sphingomonas ORF2

ATG ACG ACA GAC ATC CAC CCG GCG AGC GCC GCA TCG TCG CCG GCG GCG GCG GCG ACG ATC 60
 Met Thr Thr Asp Ile His Pro Ala Ser Ala Ala Ser Pro Ala Ala Arg Ala Thr Ile
 1 5 10 15 20
 ACC TAC AGC AAC TGC CCC GTG CCT AAT GCC CTG CTC GCC GCG CTC GGC TCA GGT ATT CTG 120
 Thr Tyr Ser Asn Cys Pro Val Pro Asn Ala Leu Leu Ala Ala Leu Gly Ser Gly Ile Leu
 25 30 35 40
 GAC AGT GCC GGG ATC ACA CTT GCC CTG CTG ACC GGA AAG CAG GGC GAG GTG CAC TTC ACC 180
 Asp Ser Ala Gly Ile Thr Leu Ala Leu Thr Gly Lys Gln Gly Glu Val His Phe Thr
 45 50 55 60
 TAC GAC CGA GAT GAC TAC ACC CGC TTC GGC GGC GAG ATT CCG CCG CTG CTC AGC GAG GGA 240
 Tyr Asp Arg Asp Tyr Thr Arg Phe Gly Gly Glu Ile Pro Pro Leu Val Ser Glu Gly
 65 70 75 80
 CTG CGT GCG CCG GGG CCG ACC CGC CTG CTG GGA CTG ACG CCG CTG GGC CCG TGG GGC 300
 Leu Arg Ala Pro Gly Arg Thr Arg Leu Leu Gly Leu Thr Pro Val Leu Gly Arg Trp Gly
 85 90 95 100
 TAC TTC GTC CCG GGC GAC AGC GCG ATC CGC ACC CGC GCC GAT CTT GCC GGC CCG CCG GTC 360
 Tyr Phe Val Arg Gly Asp Ser Ala Ile Arg Thr Pro Ala Asp Leu Ala Gly Arg Arg Val
 105 110 115 120
 GGA GTA TCC GAT TCG GCC AGG AGG ATA TTG ACC GGA AGG CTG GGC GAC TAC CGC GAA CTT 420
 Gly Val Ser Asp Ser Ala Arg Arg Ile Leu Thr Gly Arg Leu Gly Asp Tyr Arg Glu Leu
 125 130 135 140

FIG. 2A

Sphingomonas ORF2 (cont)

GAT CCC TGG CGG CAG ACC CTG GTC GCG CTG GGG ACA TGG GAG GCG CGT GCC TTG CTG AGC	480
Asp Pro Trp Arg Gln Thr Leu Val Ala Leu Gly Thr Trp Glu Ala Arg Ala Leu Ser	150
145	155
160	
ACG CTC GAG ACG GCG GGG CTT GGC GTC GGC GAC GTC GAG CTG ACG CGC ATC GAG AAC CCG	540
Thr Leu Glu Thr Ala Gly Leu Gly Val Gly Asp Val Glu Leu Thr Arg Ile Glu Asn Pro	170
165	175
180	
TTC GTC GAC GTG CCG ACC GAA CGA CTG CAT GCC GGC TCG CTC AAA GGA ACC GAC CTG	600
Phe Val Asp Val Pro Thr Glu Arg Leu His Ala Ala Gly Ser Leu Lys Gly Thr Asp Leu	190
185	195
200	
TTC CCC GAC GTG ACC AGC CAG CAG GCC GCA GTC CTT GAG GAT GAG CGC GCC GAC GCC CTG	660
Phe Pro Asp Val Thr Ser Gln Gln Ala Ala Val Leu Glu Asp Glu Arg Ala Asp Ala Leu	210
205	215
220	
TTC GCG TGG CTT CCC TGG GCG GCC GAG CTC GAG ACC CGC ATC GGT GCA CCG CCG GTC CTA	720
Phe Ala Trp Leu Pro Trp Ala Ala Glu Leu Glu Thr Arg Ile Gly Ala Arg Pro Val Leu	230
225	235
240	
GAC CTC AGC GCA GAC GAC CGC AAT GCC TAT GCG AGC ACC TGG ACG GTG AGC GCC GAG CTG	780
Asp Leu Ser Ala Asp Arg Asp Arg Asn Ala Tyr Ala Ser Thr Trp Thr Val Ser Ala Glu Leu	250
245	255
260	
GTG GAC CCG CAG CCC GAA CTG GTG CAG CGG CTC GTC GAT GCC GTG GAT GCA GGG CCG	840
Val Asp Arg Gln Pro Glu Leu Val Gln Arg Leu Val Asp Ala Val Val Asp Ala Gly Arg	270
265	275
280	

FIG. 2B

Sphingamonas ORF2

TGG GCC GAG GCC AAT GGC GAT GTC GTC TCC CGC CTG CAC GCC GAT AAC CTC GGT GTC AGT 900
 Trp Ala Glu Ala Asn Gly Asp Val Val Ser Arg Leu His Ala Asp Asn Leu Gly Val Ser 300
 280 285 290
 CCC GAA AGC GTC CGC CAG GGA TTC GGA GCC GAT TTT CAC CGC CTG ACG CCG CGG CTC 960
 Pro Glu Ser Val Arg Gln Gly Phe Gly Ala Asp Phe His Arg Arg Leu Thr Pro Arg Leu 320
 305 310 315
 GAC AGC GAT GCT ATC GCC ATC CTG GAG CGT ACT CAG CGG TTC CTG AAG GAT GCG AAC CTG 1020
 Asp Ser Asp Ala Ile Ala Ile Leu Glu Arg Thr Gln Arg Phe Leu Lys Asp Ala Asn Leu 340
 325 330 335
 ATC GAT CGG TCG TTG GCG CTC GAT CGG TGG GCT GCA CCT GAA TTC CTC GAA CAA AGT CTC 1080
 Ile Asp Arg Ser Leu Ala Leu Asp Arg Trp Ala Ala Pro Glu Phe Leu Glu Gln Ser Leu 360
 345 350 355
 TCA CGC CAG GTC GAA GGG CAG ATA GCA TGA
 Ser Arg Gln Val Glu Gly Gln Ile Ala 370
 365

FIG. 2C

Sphingomonas ORF3

ATG AAC GAA CTC GTC AAA GAT CTC GGC CTC AAT CGA TCC GAT CCG ATC GGC GCT GTG CGG 60
 Met Asn Glu Leu Val Lys Asp Leu Gly Leu Asn Arg Ser Asp Pro Ile Gly Ala Val Arg 20
 1 5 10 15 20
 CGA CTG GCC GCG CAG TGG GGG GCC ACC GCT GTT GAT CGG GAC CCG GCC GGC GGA TCG GCA 120
 Arg Leu Ala Ala Gln Trp Gly Ala Thr Ala Val Asp Arg Asp Arg Ala Gly Gly Ser Ala 40
 25 30 35 40
 ACC GCC GAA CTC GAT CAA CTG CGC GGC AGC GGC CTG CTC TCG CTG TCC ATT CCC GCC GCA 180
 Thr Ala Glu Leu Asp Gln Leu Arg Gly Ser Gly Leu Ser Leu Ser Ile Pro Ala Ala 60
 45 50 55 60
 TAT GGC GGC TGG GGC GAC TGG CCA ACG ACT CTG GAA GTT ATC CGC GAA GTC GCA ACG 240
 Tyr Gly Gly Trp Gly Ala Asp Trp Pro Thr Thr Leu Glu Val Ile Arg Glu Val Ala Thr 80
 65 70 75 80
 GTG GAC GGA TCG CTG GCG CAT CTA TTC GGC TAC CAC CTC GGC TGC GTA CCG ATG ATC GAG 300
 Val Asp Gly Ser Leu Ala His Leu Phe Gly Tyr His Leu Gly Cys Val Pro Met Ile Glu 100
 85 90 95 100
 CTG TTC GGC TCG GCG CCA CAA AAG GAA CCG CTG TAC CGC CAG ATC GCA AGC CAT GAT TGG 360
 Leu Phe Gly Ser Ala Pro Gln Lys Glu Arg Leu Tyr Arg Gln Ile Ala Ser His Asp Trp 120
 105 110 115 120
 CCG GTC GGC AAT GCG TCG AGC GAA AAC AAC AGC CAC GTG CTC GAG TGG AAG CTT GCC GCC 420
 Arg Val Gly Asn Ala Ser Ser Glu Asn Asn Ser His Val Leu Glu Trp Lys Leu Ala Ala 140
 125 130 135 140

FIG. 3A

SPHINGOMONAS orf3 (cont)

ACC GCC GTC GAT GAT GGC GGG TTC GTC CTC AAC GGC GCG AAG CAC TTC TGC AGC GGC GCC	480
Thr Ala Val Asp Asp 145	
150	
155	
160	
AAA AGC TCC GAC CTG CTC ATC GTG TTC GGC GTG ATC CAG GAC GAA TCC CCC CTG CGC GGC	540
Lys Ser Ser Asp Leu Leu Ile Val Phe Gly Val Ile Gln Asp Glu Ser Pro Leu Arg Gly	
165	
170	
175	
180	
GCG ATC ATC ACC GCG GTC ATC ACC ACC GAC GGC GGC GGT GTT CAG ATC AAT GAC GAC TGG	600
Ala Ile Ile Thr Ala Val Ile Pro Thr Asp Arg Ala Gly Val Gln Ile Asn Asp Asp Trp	
185	
190	
195	
200	
CGC GCA ATC GGG ATG CGC CAG ACC GAC ACC GGC AGC GCC GAA TTT CGC GAC GTC CGA GTC	660
Arg Ala Ile Gly Met Arg Gln Thr Asp Ser Gly Ser Ala Glu Phe Arg Asp Val Arg Val	
205	
210	
215	
220	
TAC CCA GAC GAG ATC TTG GGG GCA CCA AAC TCA GTC GTT GAG GCG TTC GTG ACA AGC AAC	720
Tyr Pro Asp Glu Ile Leu Gly Ala Pro Asn Ser Val Val Glu Ala Phe Val Thr Ser Asn	
225	
230	
235	
240	
CGC GGC AGC CTG TGG ACG CCG CCG ATT CAG TCG ATC TTC TCG AAC GTT TAT CTG GGG CTC	780
Arg Gly Ser Leu Trp Thr Pro Ala Ile Gln Ser Ile Phe Ser Asn Val Tyr Leu Gly Leu	
245	
250	
255	
260	
GCG CGT GGC CTC GAG GCG GCA GCG GAT TAC ACC CGG ACC CAG AGC CGC CCC TGG ACA	840
Ala Arg Gly Ala Leu Glu Ala Ala Asp Tyr Thr Arg Thr Gln Ser Arg Pro Trp Thr	
265	
270	
275	
280	

FIG. 3B

Sphingomonas ORF3 (cont.)

CCC GCC GGC GTG GCG AAG GCG ACA GAG GAT CCC CAC ATC ATC GCC ACC TAC GGT GAA CTG	900
Pro Ala Gly Val Ala Lys Ala Thr Glu Asp Pro His Ile Ile Ala Thr Tyr Gly Glu Leu	300
285	295
GCG ATC GCG CTC CAG GGC GCG GCG GAG GCG GGC GCG CTC GCG CTC TTG CAA CAG	960
Ala Ile Ala Leu Gln Gly Ala Glu Ala Ala Arg Glu Val Ala Ala Leu Leu Gln Gln	320
305	315
GCG TGG GAC AAG GGC GAT GCG GTG ACG CCC GAA GAG CGC GGC CAG CTG ATG GTG AAG GTT	1020
Ala Trp Asp Lys Gly Asp Ala Val Thr Pro Glu Glu Arg Gly Gln Leu Met Val Lys Val	340
325	335
TCG GGT GTG AAG GCC CTC TCG ACG AAG GCC GCG CTC GAC ATC ACC AGC CGT ATT TTC GAG	1080
Ser Gly Val Lys Ala Leu Ser Thr Lys Ala Ala Leu Asp Ile Thr Ser Arg Ile Phe Glu	360
345	355
ACA ACG GGC TCG CGA TCG ACG CAT CCC AGA TAC GGA TTC GAT CGG TTC TGG CGT AAC ATC	1140
Thr Thr Gly Ser Arg Ser Thr His Pro Arg Tyr Gly Phe Asp Arg Phe Trp Arg Asn Ile	380
365	375
CGG ACT CAT ACG CTG CAC GAT CCG GTA TCG TAT AAA ATC GTC GAT GTG GGG AAC TAC ACG	1200
Arg Thr His Thr Leu His Asp Pro Val Ser Tyr Lys Ile Val Asp Val Gly Asn Tyr Thr	400
385	395
CTC AAC GGG ACA TTC CCG GTT CCC GGA TTT ACG TCA	
Leu Asn Gly Thr Phe Pro Val Pro Gly Phe Thr Ser	410
405	

FIG. 3C

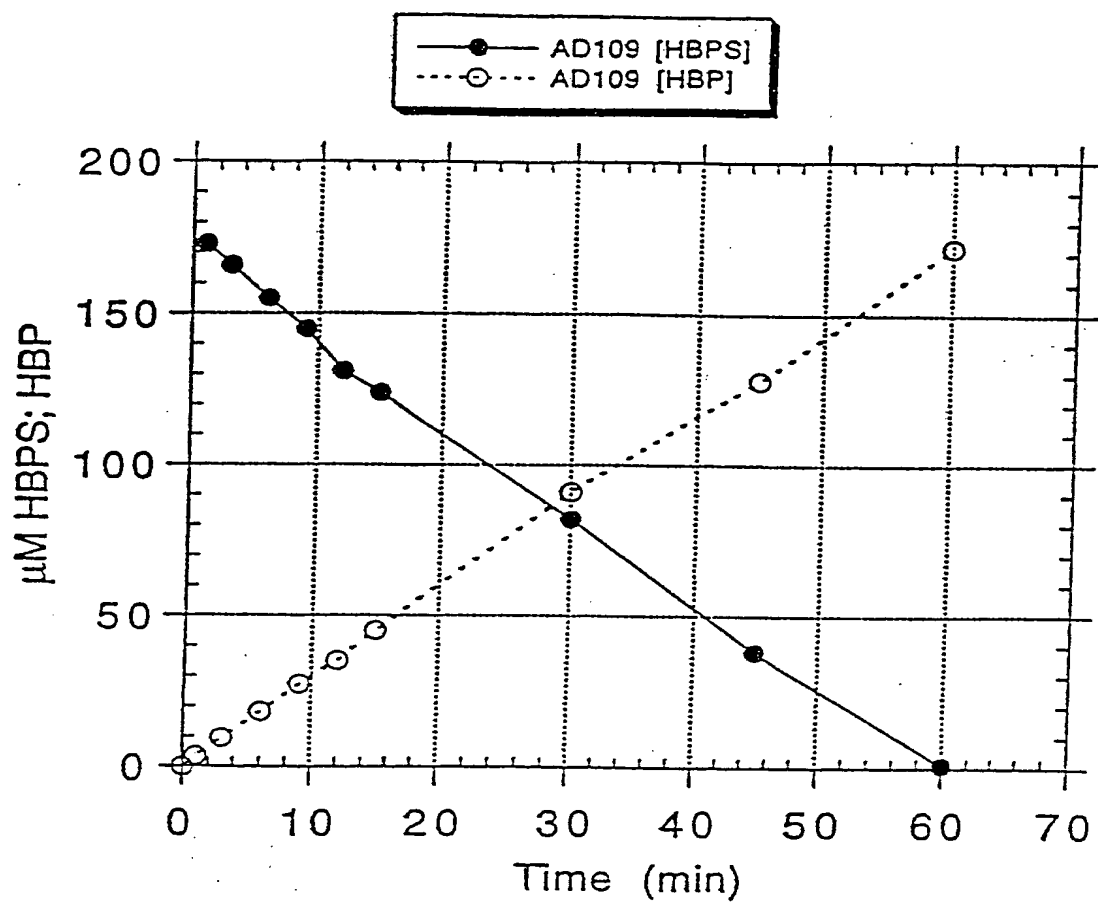


FIG. 4

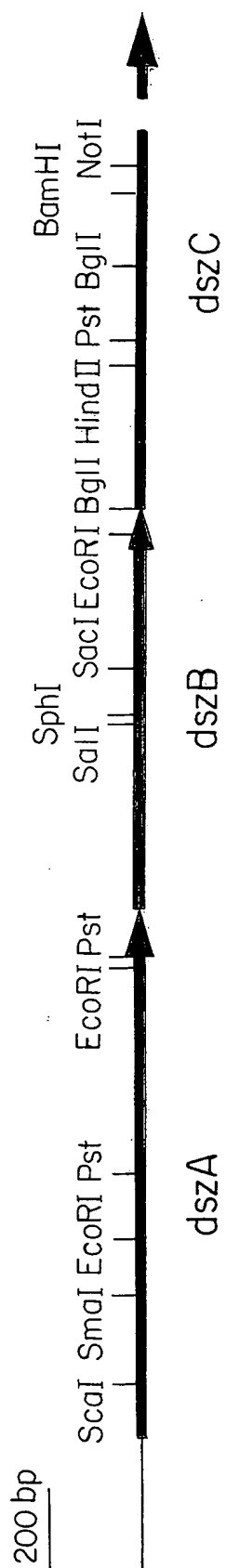


FIG. 5

Sphingomonas dsz sequence

GGTTCGAGAT	CGATCTGACC	GTCGAACCCG	GCGCGGTTCA	AACCATCCTC	TGGGGCCTCT	60
CCAAGCTCTA	GCTAGACTGG	CAGCTTGGGC	CGCGCCAAGT	TTGGTAGGAG	ACCCCGGAGA	
TCTTGCACTT	GACATAGGAA	TCTCTACTAA	ATAAATAGAT	ATTTATTCTGA	CACTAAGTTC	120
AGAACGTGAA	CTGTATCCTT	AGAGATGATT	TATTTATCTA	TAAATAAGCT	GTGATTCAAG	
GGTGATCAGG	CCGACCGTGT	GTCTCAAGTG	CTCGCTCCGG	GTTGCCACGA	GCTAAAGCGC	180
CCACTAGTCC	GGCTGGCACA	CAGAGTTCAC	GAGCGAGGCC	CAACGGTGCT	CGATTTTCGCG	
GCGATGCTGG	GGCGACAGCG	CTAGGCATTG	CGTTCCCTCA	CACCAATGAT	GAGATGATAC	240
CGCTACGACC	CCGCTGTGCG	GATCCGTAAC	GCAAGGGAGT	GTGGTTACTA	CTCTACTATG	
GATGCGCATG	ACCACTATCC	GCACCTAGCA	CGAAAGATCC	GTGCATTTTCG	CGAATGCCAA	300
CTACGCGTAC	TGGTGATAGG	CGTGGATCGT	GCTTTCTAGG	CACGTAAAGC	GCTTACGGTT	
TGAAGAGGAC	CGACGTACGG	CAGCTTCCTA	CGCTTTTCGCG	CCATCGTTCA	TAGCCAAGGT	360
ACTTCTCCTG	GCTGCATGCC	GTCGAAGGAT	GCGAAAGCGC	GGTAGCAAGT	ATCGGTTCCA	
CTTTTCGACG	CCGGTTTCGCG	TGGGCGACTG	ACGGCGGTTAG	CGCCGCGACT	ATTCGTTTCA	420
GAAAAGCTGC	GGCCAAGCGC	ACCCGCTGAC	TGCCGCCATC	GCGGCGCTGA	TAAGCAAAGT	
AACTCACGAG	GATAAGAGCC	TATGACCGAT	CCACGTCAGC	TGCACCTGGC	CGGATTCTTC	480
TTGAGTGCTC	CTATTCTCGG	ATACTGGCTA	GGTGCACTCG	ACGTGGACCG	GCCTAAGAAG	
TGTGCCGGCA	ACGTCACGCA	CGCCACGGA	GCGTGGCGCC	ACGCCGACGA	CTCCAACGGC	540
ACACGGCCGT	TGCAGTGCGT	GCGGGTGCCT	CGCACC GCGG	TGCGGCTGCT	GAGGTTGCCG	
TTCCTACCA	AGGAGTACTA	CCAGCAGATT	GCCCCGACGC	TCGAGCGCGG	CAAGTTCGAC	600
AAGGAGTGGT	TCCTCATGAT	GGTCGTCTAA	CGGGCGTGCG	AGCTCGCGCC	GTTCAAGCTG	

FIG. 6A

Sphingomonas dsz sequence (cont)

CTGCTGTTCC TTCCCGACGC GCTCGCCGTG TGGGACAGCT ACGGCGACAA TCTGGAGACC	660
GACGACAAGG AAGGGCTGCG CGAGCGGCAC ACCCTGTCGA TGCCGCTGTT AGACCTCTGG	
GGTCTGCGGT ATGGCGGGCA AGGCGCGGTG ATGCTGGAGC CCGGCGTAGT TATCGCCGCG	720
CCAGACGCCA TACCGCCCCT TCCGCGCCAC TACGACCTCG GGCCGCATCA ATAGCGGCGC	
ATGGCCTCGG TGACCGAACA TCTGGGGCTG GGCGCCACCA TTTCCACCAC CTACTACCCG	780
TACCGGAGCC ACTGGCTTGT AGACCCCGAC CCGCGGTGGT AAAGGTGGTG GATGATGGGC	
CCCTACCATG TAGCCCGGGT CGTCGCTTCG CTGGACCAGC TGTCCTCCGG GCGAGTGTCG	840
GGGATGGTAC ATCGGGCCCA GCAGCGAAGC GACCTGGTCG ACAGGAGGCC CGCTCACAGC	
TGGAACGTGG TCACCTCGCT CAGCAATGCA GAGGCGCGCA ACTTCGGCTT CGATGAACAT	900
ACCTTGCAAC AGTGGAGCGA GTCGTTACGT CTCCGCGCGT TGAAGCCGAA GCTACTTGTA	
CTCGACCACG ATGCCCCTA CGATCGCGCC GATGAATTCC TCGAGGTCGT GCGCAAGCTC	960
GAGCTGGTGC TACGGGCGAT GCTAGCGCGG CTACTTAAGG AGCTCCAGCA CGCGTTCGAG	
TGGAACAGCT GGGATCGCGA TCGCTGACA CTCGACAAGG CAACCGGCCA GTTCGCCGAT	1020
ACCTTGTCGA CCTAGCGCT ACGCGACTGT GAGCTGTTCC GTTGGCCGGT CAAGCGGCTA	
CCGGCTAAGG TCGCTACAT CGACCACCGC GGCGAATGGC TCAACGTACG CGGGCCGCTT	1080
GGCCGATTCC ACGCGATGTA GCTGGTGGCG CCGCTTACCG AGTTGCATGC GCCCGGCGAA	
CAGGTGCCGC GCTCCCCCA GGGCGAGCCT GTCATTCTGC AGGCCGGGCT TTCGGCGCGG	1140
GTCCACGGCG CGAGGGGGGT CCCGCTCGGA CAGTAAGACG TCCGGCCCGA AAGCCGCGCC	
GGCAAGCGCT TCGCCGGGCG CTGGGCGGAC GCGGTGTTCA CGATTTGCCC CAATCTGGAC	1200
CCGTTGCGCA AGCGGCCCCG GACCCGCCTG CGCCACAAGT GCTAAAGCGG GTTAGACCTG	

FIG. 6B

Sphingomonas dsz sequence (cont)

ATCATGCAGG	CCACGTACCG	CGACATAAAG	GCGCAGGTCG	AGGCCGCCGG	ACGCGATCCC	1260
TAGTACGTCC	GGTGCAATGGC	GCTGTATTTT	CGCGTCCAGC	TCCGGCGGCC	TGCGCTAGGG	
GAGCAGGTCA	AGGTGTTTGC	CGCGGTGATG	CCGATCCTCG	GCGAGACCGA	GGCGATCGCC	1320
CTCGTCCAGT	TCCACAAACG	GCGCCACTAC	GGCTAGGAGC	CGCTCTGGCT	CCGCTAGCGG	
AGGCAGCGTC	TCGAATACAT	AAATTGCTG	GTGCATCCCG	AAGTCGGGCT	TTCTACGTTG	1380
TCCGTCGCAG	AGCTTATGTA	TTTAAGCGAC	CACGTAGGGC	TTCAGCCCGA	AAGATGCAAC	
TCCAGCCATG	TCGGGGTCAA	CCTTGCCGAC	TATTCGCTCG	ATACCCCGCT	GACCGAGGTC	1440
AGGTCGGTAC	AGCCCCAGTT	GGAACGGCTG	ATAAGCGAGC	TATGGGGCGA	CTGGCTCCAG	
CTGGGCGATC	TCGCCCAGCG	CAACGTGCCC	ACCCAACCTGG	GCATGTTCGC	CAGGATGTTG	1500
GACCCGCTAG	AGCGGGTCGC	GTTGCACGGG	TGGGTTGACC	CGTACAAGCG	GTCCTACAAC	
CAGGCCGAGA	CGCTGACCGT	GGGAGAAATG	GGCCGGCGTT	ATGGCGCCAA	CGTGGGCTTC	1560
GTCCGGCTCT	GCGACTGGCA	CCCTCTTTAC	CCGGCCGCAA	TACCGCGGTT	GCACCCGAAG	
GTCCCGCAGT	GGGCGGGAAC	CCGCGAGCAG	ATCGCGGACC	TGATCGAGAT	CCATTTCAAG	1620
CAGGGCGTCA	CCCGCCCTTG	GGCGCTCGTC	TAGCGCCTGG	ACTAGCTCTA	GGTAAAGTTC	
GCCGGCGGCG	CCGATGGCTT	CATCATCTCG	CCGGCGTTCC	TGCCCCGATC	TTACGAGGAA	1680
CGGCCGCCGC	GGCTACCGAA	GTAGTAGAGC	GGCCGCAAGG	ACGGGCCTAG	AATGCTCCTT	
TTCGTCGATC	AGGTGGTGCC	CATCCTGCAG	CACCGCGGAC	TGTTCCGCAC	TGATTACGAA	1740
AAGCAGCTAG	TCCACCACGG	GTAGGACGTC	GTGGCGCCTG	ACAAGGCGTG	ACTAATGCTT	
GGCCGCACCC	TGCGCAGCCA	TCTGGGACTG	CGTGAAACCG	CATACCTGGG	AGAGTACGCA	1800
CCGGCGTGGG	ACGCGTCGGT	AGACCCTGAC	GCACTTGGGC	GTATGGACCC	TCTCATGCGT	

FIG. 6C

Sphingomonas dsz sequence (cont)

TGACGACAGA	CATCCACCCG	GCGAGCGCCG	CATCGTCGCC	GGCGGCGCGC	GCGACGATCA	1860
ACTGCTGTCT	GTAGGTGGGC	CGCTCGCGGC	GTAGCAGCGG	CCGCCGCGCG	CGCTGCTAGT	
CCTACAGCAA	CTGCCCCGTG	CCTAATGCCC	TGCTCGCCGC	GCTCGGCTCA	GGTATTCTGG	1920
GGATGTCGTT	GACGGGGCAC	GGATTACGGG	ACGAGCGGCG	CGAGCCGAGT	CCATAAGACC	
ACAGTGCCGG	GATCACACTT	GCCCTGCTGA	CCGGAAAGCA	GGGCGAGGTG	CACTTCACCT	1980
TGTCACGGCC	CTAGTGTGAA	CGGGACGACT	GGCCTTTCTG	CCCGCTCCAC	GTGAAGTGA	
ACGACCGAGA	TGACTACACC	CGCTTCGGCG	GCGAGATTCC	GCCGCTGGTC	AGCGAGGGAC	2040
TGCTGGCTCT	ACTGATGTGG	GCGAAGCCGC	CGCTCTAAGG	CGGCGACCAG	TCGCTCCCTG	
TGCGTGCGCC	GGGGCGGACC	CGCCTGCTGG	GACTGACGCC	GGTGCTGGGC	CGCTGGGGCT	2100
ACGCACGCGG	CCCCGCCTGG	GCGGACGACC	CTGACTGCGG	CCACGACCCG	GCGACCCCGA	
ACTTCGTCCG	GGGCGACAGC	GCGATCCGCA	CCCCGGCCGA	TCTTGCCGGC	CGCCGCGTCG	2160
TGAAGCAGGC	CCCGCTGTCT	CGCTAGGCGT	GGGGCCGGCT	AGAACGGCCG	GCGGCGCAGC	
GAGTATCCGA	TTCGGCCAGG	AGGATATTGA	CCGGAAGGCT	GGGCGACTAC	CGCGAACTTG	2220
CTCATAGGCT	AAGCCGGTCC	TCCTATAACT	GGCCTTCCGA	CCCGCTGATG	GCGCTTGAAC	
ATCCCTGGCG	GCAGACCCTG	GTCGCGCTGG	GGACATGGGA	GGCGCGTGCC	TTGCTGAGCA	2280
TAGGGACCGC	CGTCTGGGAC	CAGCGCGACC	CCTGTACCCT	CCGCGCACGG	AACGACTCGT	
CGCTCGAGAC	GGCGGGGCTT	GGCGTCGGCG	ACGTCGAGCT	GACGCGCATC	GAGAACCCGT	2340
GCGAGCTCTG	CCGCCCCGAA	CCGCAGCCGC	TGCAGCTCGA	CTGCGCGTAG	CTCTTGGGCA	
TCGTGACGT	GCCGACCGAA	CGACTGCATG	CCGCCGGCTC	GCTCAAAGGA	ACCGACCTGT	2400
AGCAGCTGCA	CGGCTGGCTT	GCTGACGTAC	GGCGGCCGAG	CGAGTTTCCT	TGGCTGGACA	

FIG. 6D

Sphingomonas dsz sequence (cont)

TCCCCGACGT	GACCAGCCAG	CAGGCCGCAG	TCCTTGAGGA	TGAGCGCGCC	GACGCCCTGT	2460
AGGGGCTGCA	CTGGTCGGTC	GTCCGGCGTC	AGGAACTCCT	ACTCGCGCGG	CTGCGGGACA	
TCGCGTGGCT	TCCCTGGGCG	GCCGAGCTCG	AGACCCGCAT	CGGTGCACGG	CCGGTCCTAG	2520
AGCGCACCGA	AGGGACCCGC	CGGCTCGAGC	TCTGGGCGTA	GCCACGTGCC	GCCCAGGATC	
ACCTCAGCGC	AGACGACCGC	AATGCCTATG	CGAGCACCTG	GACGGTGAGC	GCCGAGCTGG	2580
TGGAGTCGCG	TCTGCTGGCG	TTACGGATAC	GCTCGTGGAC	CTGCCACTCG	CGGCTCGACC	
TGGACCGGCA	GCCCCGAAGT	GTGCAGCGGC	TCGTGATGTC	CGTGGTGGAT	GCAGGGCGGT	2640
ACCTGGCCGT	CGGGCTTGAC	CACGTCGCCG	AGCAGCTACG	GCACCACCTA	CGTCCCGCCA	
GGGCCGAGGC	CAATGGCGAT	GTCGTCTCCC	GCCTGCACGC	CGATAACCTC	GGTGTGAGTC	2700
CCCGGCTCCG	GTTACCGCTA	CAGCAGAGGG	CGGACGTGCG	GCTATTGGAG	CCACAGTCAG	
CCGAAAGCGT	CCGCCAGGGA	TTCGGAGCCG	ATTTTCACCG	CCGCCTGACG	CCGCGGCTCG	2760
GGCTTTCCGA	GGCGGTCCCT	AAGCCTCGGC	TAAAAGTGCC	GGCGGACTGC	GGCGCCGAGC	
ACAGCGATGC	TATCGCCATC	CTGGAGCGTA	CTCAGCGGTT	CCTGAAGGAT	GCGAACCTGA	2820
TGTCGCTACG	ATAGCGGTAG	GACCTCGCAT	GAGTCGCCAA	GGACTTCCTA	CGCTTGGAAT	
TCGATCGGTC	GTTGGCGCTC	GATCGGTGGG	CTGCACCTGA	ATTCCTCGAA	CAAAGTCTCT	2880
AGCTAGCCAG	CAACCGCGAG	CTAGCCACCC	GACGTGGACT	TAAGGAGCTT	GTTTCAGAGA	
CACGCCAGGT	CGAAGGGCAG	ATAGCATGAA	CGAACTCGTC	AAAGATCTCG	GCCTCAATCG	2940
GTGCGGTCCA	GCTTCCCGTC	TATCGTACTT	GCTTGAGCAG	TTTCTAGAGC	CGGAGTTAGC	
ATCCGATCCG	ATCGGCGCTG	TGCGGCGACT	GGCCGCGCAG	TGGGGGGCCA	CCGCTGTTGA	3000
TAGGCTAGGC	TAGCCGCGAC	ACGCCGCTGA	CCGGCGCGTC	ACCCCCCGGT	GGCGACAAC	

FIG. 6E

Sphingomonas dsz sequence (cont)

TCGGGACCGG	GCCGGCGGAT	CGGCAACCGC	CGAACTCGAT	CAACTGCGCG	GCAGCGGCCT	3060
AGCCCTGGCC	CGGCCGCCTA	GCCGTTGGCG	GCTTGAGCTA	GTTGACGCGC	CGTCGCCGGA	
GCTCTCGCTG	TCCATTCCCG	CCGCATATGG	CGGCTGGGGC	GCCGACTGGC	CAACGACTCT	3120
CGAGAGCGAC	AGGTAAGGGC	GGCGTATACC	GCCGACCCCG	CGGCTGACCG	GTTGCTGAGA	
GGAAGTTATC	CGCGAAGTCG	CAACGGTGGA	CGGATCGCTG	GCGCATCTAT	TCGGCTACCA	3180
CCTTCAATAG	GCGCTTCAGC	GTTGCCACCT	GCCTAGCGAC	CGCGTAGATA	AGCCGATGGT	
CCTCGGCTGC	GTACCGATGA	TCGAGCTGTT	CGGCTCGGCG	CCACAAAAGG	AACGGCTGTA	3240
GGAGCCGACG	CATGGCTACT	AGCTCGACAA	GCCGAGCCGC	GGTGTTTTCC	TTGCCGACAT	
CCGCCAGATC	GCAAGCCATG	ATTGGCGGGT	CGGGAATGCG	TCGAGCGAAA	ACAACAGCCA	3300
GGCGGTCTAG	CGTTCGGTAC	TAACCGCCCA	GCCCTTACGC	AGCTCGCTTT	TGTTGTCGGT	
CGTGCTCGAG	TGGAAGCTTG	CCGCCACCGC	CGTCGATGAT	GGCGGGTTTCG	TCCTCAACGG	3360
GCACGAGCTC	ACCTTCGAAC	GGCGGTGGCG	GCAGCTACTA	CCGCCCAAGC	AGGAGTTGCC	
CGCGAAGCAC	TTCTGCAGCG	GCGCCAAAAG	CTCCGACCTG	CTCATCGTGT	TCGGCGTGAT	3420
GCGCTTCGTG	AAGACGTCGC	CGCGGTTTTT	GAGGCTGGAC	GAGTAGCACA	AGCCGCACTA	
CCAGGACGAA	TCCCCCTGC	GCGGCGCGAT	CATCACCGCG	GTCATTCCCA	CCGACCGGGC	3480
GGTCCTGCTT	AGGGGGGACG	CGCCGCGCTA	GTAGTGGCGC	CAGTAAGGGT	GGCTGGCCCC	
CGGTGTTTCA	ATCAATGACG	ACTGGCGCGC	AATCGGGATG	CGCCAGACCG	ACAGCGGCAG	3540
GCCACAAGTC	TAGTTACTGC	TGACCGCGCG	TTAGCCCTAC	GCGGTCTGGC	TGTCGCCGTC	
CGCCGAATTT	CGCGACGTCC	GAGTCTACCC	AGACGAGATC	TTGGGGGCAC	CAAACCTCAGT	3600
GCGGCTTAAA	GCGCTGCAGG	CTCAGATGGG	TCTGCTCTAG	AACCCCGTGT	GTTTGAGTCA	

FIG. 6F

Sphingomonas dsz sequence (cont)

CGTTGAGGCG	TTCGTGACAA	GCAACCGCGG	CAGCCTGTGG	ACGCCGGCGA	TTCAGTCGAT	3660
GCAACTCCGC	AAGCACTGTT	CGTTGGCGCC	GTCGGACACC	TGCGGCCGCT	AAGTCAGCTA	
CTTCTCGAAC	GTTTATCTGG	GGCTCGCGCG	TGGCGCGCTC	GAGGCGGCAG	CGGATTACAC	3720
GAAGAGCTTG	CAAATAGACC	CCGAGCGCGC	ACCGCGCGAG	CTCCGCCGTC	GCCTAATGTG	
CCGGACCCAG	AGCCGCCCCCT	GGACACCCGC	CGGCGTGGCG	AAGGCGACAG	AGGATCCCCA	3780
GGCCTGGGTC	TCGGCGGGGA	CCTGTGGGCG	GCCGCACCGC	TTCCGCTGTC	TCCTAGGGGT	
CATCATCGCC	ACCTACGGTG	AACTGGCGAT	CGCGCTCCAG	GGCGCCGAGG	CGGCCGCGCG	3840
GTAGTAGCGG	TGGATGCCAC	TTGACCGCTA	GCGCGAGGTC	CCGCGGCTCC	GCCGGCGCGC	
CGAGGTGCGG	GCCCTGTTGC	AACAGGCGTG	GGACAAGGGC	GATGCGGTGA	CGCCCGAAGA	3900
GCTCCAGCGC	CGGGACAACG	TTGTCCGCAC	CCTGTTCCCG	CTACGCCACT	GCGGGCTTCT	
GCGCGGCCAG	CTGATGGTGA	AGGTTTCGGG	TGTGAAGGCC	CTCTCGACGA	AGGCCGCCCT	3960
CGCGCCGGTC	GACTACCACT	TCAAAGCCC	ACACTTCCGG	GAGAGCTGCT	TCCGGCGGGA	
CGACATCACC	AGCCGTATTT	TCGAGACAAC	GGGCTCGCGA	TCGACGCATC	CCAGATACGG	4020
GCTGTAGTGG	TCGGCATAAA	AGCTCTGTTG	CCCGAGCGCT	AGCTGCGTAG	GGTCTATGCC	
ATTCGATCGG	TTCTGGCGTA	ACATCCGGAC	TCATACGCTG	CACGATCCGG	TATCGTATAA	4080
TAAGCTAGCC	AAGACCGCAT	TGTAGGCCTG	AGTATGCGAC	GTGCTAGGCC	ATAGCATATT	
AATCGTCGAT	GTGGGGAACT	ACACGCTCAA	CGGGACATTC	CCGGTTCCCG	GATTTACGTC	4140
TTAGCAGCTA	CACCCCTTGA	TGTGCGAGTT	GCCCTGTAAAG	GGCCAAGGGC	CTAAATGCAG	
ATGA						4144
TACT						

FIG. 6G

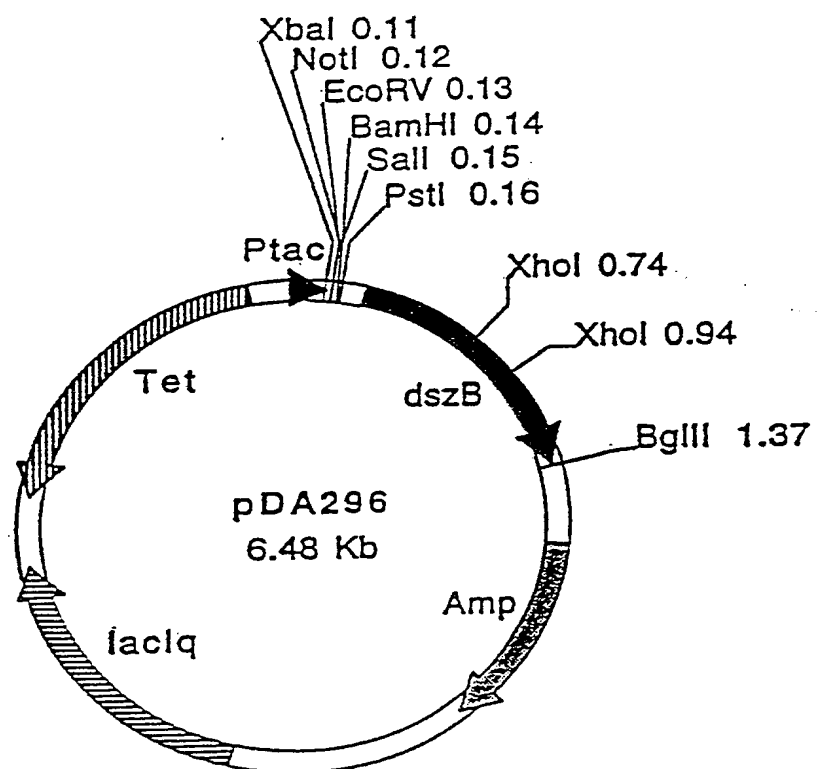


FIG. 7

DszA (S)	1	MTDPRQLHLAGFFCAGNVTHAHGAWRHADDSNGFLTKEYYQQIARTLERG	50
		: . : : . . : . :	
DszA (R)	1	MTQQRQMHLAGFFSAGNVTHAHGAWRHTDASNDFLSGKYYQHIARTLERG	50
DszA (S)	51	KFDLLFLPDALAVWDSYGDNLETGLRYGGQGAVMLEPGVVIAAMASVTEH	100
		: : : . : : . .	
DszA (R)	51	KFDLLFLPDGLAVEDSYGDNLDTGVLGGQGAVALPASVVATMAAVTEH	100
DszA (S)	101	LGLGATISTTYPPYHVARVVASLDQLSSGRVSWNVVTSLSNAEARNFGF	150
		. . . : . : :	
DszA (R)	101	LGLGATISATYPPYHVARVFATLDQLSGGRVSWNVVTSLNDAEARNFGI	150
DszA (S)	151	DEHLDHDARYDRADEFLEVVRKLWNSWDRDALTDKATGQFADPAKVRYI	200
		: : : . : . . : :	
DszA (R)	151	NQHLEHDARYDRADEFLEAVKKLWNSWDEDALVLDKAAGVFADPAKVHYV	200
DszA (S)	201	DHRGEWLNVRGPLQVPRSPQGEPVILQAGLSARGKRFAGRWADAVFTISP	250
		: : : : : . . .	
DszA (R)	201	DHHGEWLNVRGPLQVPRSPQGEPVILQAGLSPRGRRFAGKWAEAVFSLAP	250
DszA (S)	251	NLDIMQATYRDIKAQVEAAGRDPQVQVFAAVMPILGETEAIARQRLEYI	300
		: : . : : : : . : . : . : : :	
DszA (R)	251	NLEVMQATYQGIKAEVDAAGRDPDQTKIFTAVMPVLGESQAVAQERLEYL	300
DszA (S)	301	NSLVHPEVGLSTLSSHVGVNLDYSLDTPLTEVLGDLAQRNVPTQLGMFA	350
		. : . . : : : . :	
DszA (R)	301	NSLVHPEVGLSTLSSHTGINLAAYPLDTPIKDILRDLQDRNVPTQLHMFA	350
DszA (S)	351	RMLQAETLTVGEMGRRYGANVGFPQWAGTREQIADLIEIHFKAGGADGF	400
		: . . : : . : . : :	
DszA (R)	351	AATHSEELTLAEMGRRYGTNVGFPQWAGTREQIADLIEIHFKAGGADGF	400
DszA (S)	401	IISPAFLPGSYEEFVDQVVPILQHRGLFRTDYEGRTLRLSHLGLREPAYLG	450
		: : . . : : 	
DszA (R)	401	IISPAFLPGSYDEFVDQVVPVLQDRGYFRTEYQGNTLRDHLGLRVPQLQG	450
DszA (S)	451	EYA 453	
		: .	
DszA (R)	451	QPS 453	

FIG. 8

DszB	(S)	MTTDIHPASAASSPAA--RATITYSNCPVPNALLAALGSGILDSAGITLALL	50
DszB		MTSRVDPANPGSELDISAIRDTLTYSNCPVPNALLTASESGFLDAAGIELDVL	52
DszB	(S)	TGKQGEVHFTYDRDDYTRFGGEIPPLVSEGLRAPGRTRLLGLTPVLGRWGYF	102
DszB		SGQQGTIVHFTYDQPAYTRFGGEIPPLLSEGLRAPGRTRLLGITPLLGRQGFF	104
DszB	(S)	VRGDSAIRTPADLAGRRVGVSDSARRILTGRIGDYRELDPWRQTLVALGTWE	154
DszB		VRDDSPITAAADLAGRRIGVSASAIRILRGQLGDYLELDPWRQTLVALGSWE	156
DszB	(S)	ARALLSTLETAGLGVGDVELTRLENPFVDVPTERLHAAGSLKGTDLFPDVT	206
DszB		ARALLHTLEHGELGVDDVELVPISSPGVDVPAEQLEESATVKGADLFPDVAR	208
DszB	(S)	QOAAVLEDERADALEAWLPWAAELETRIGARPVLDLSADDRNAYASTWTVSA	258
DszB		GQAAVLASGDVDALYSWLPWAGELQA-TGARPVVDLGLDERNAYASVWTVSS	260
DszB	(S)	ELVDRQPELVQRLVDAVVDAGRWAEANGDVVSRLHADNLGVSPESVRQGFGA	310
DszB		GLVRQRPGLVQRLVDAAVDAGLWARDHSDAVTSLHAANLGVSTGAVGQFGA	312
szB	(S)	DFHRRLTPRLDSDAIAILERTQRFLKDANLIDRSLALDRWAAPEFLEQSLSRQVEGQIA	369
DszB		DFQQLVPRLDHDALALLERTQQFLTNLLQEPVALDQWAAPEFLNNSLNRHR	365

FIG. 9

DszC (S)	1MNELVKDLGLNRS DPIGAVRRLAAQWGATAVDRDRAGGSATAELD	45
DszC (R)	1	MTLSPEKQHVRPRDAADNDP VAVARGLA EKWRATAVERDRAGGSATAERE	50
DszC (S)	46	QLRGSGLLSLSIPAAYGGWGADWPTTLEVIREVATVDGSLAHLFGYHLGC	95
DszC (R)	51	DLRASALLSLLVPREYGGWGADWPTAIEVVREIAAADGSLGHLFGYHLTN	100
DszC (S)	96	VPMIELFGSAPQKERLYRQIASHDWRVGNASSENNSHVLEWKLAATAVDD	145
DszC (R)	101	APMIELIGSQEQEEHLYTQIAQNNWWTGNASSENNSHVLDWKVSATPTED	150
DszC (S)	146	GGFVLNGAKHFCSGAKSSDLLIVFGVIOQDESPLRGAIITAVIPTDRAGVQ	195
DszC (R)	151	GGYVLNGTKHFCSGAKGSDLLFVFGVVQDDSPQQGAIIAAAIPTSRAGVT	200
DszC (S)	196	INDDWRAIGMRQTDSGSAEFRDVRVYPDEILGAPNSVVEAFVTSNRGSLW	245
DszC (R)	201	PNDDWAAIGMRQTDSGSTDFHNVKVEPDEV LGAPNAFVLAFIQSERGSLF	250
DszC (S)	246	TPAIQSIFSNVYLGLARGALEAAAADYTRTQSRPWT PAGVAKATEDPHIIA	295
DszC (R)	251	APIAQLIFANVYLGIAHGALDAAREYTRTQARPWT PAGIQQATEDPYTIR	300
DszC (S)	296	TYGELAIALQGAEEAAAREVAALLQQAWDKGD AVTPEERGQLMVKVS GVKA	345
DszC (R)	301	SYGEFTIALQGA DAAAREAAHLLQTVWDKGDALTPEDRGELMVKVS GVKA	350
DszC (S)	346	LSTKAALDITSRIFETTGSRSTHPRYGFDRFWRNIR THTLHDPVSYKIVD	395
DszC (R)	351	LATNAALNISSGVFEVIGARGTHPRYGFDRFWRNV RTHSLHDPVSYKIAD	400
DszC (S)	396	VGNYTLNGTFPVP GFTS	412
DszC (R)	401	VGKHTLNGQYPI P GFTS	417

FIG. 10

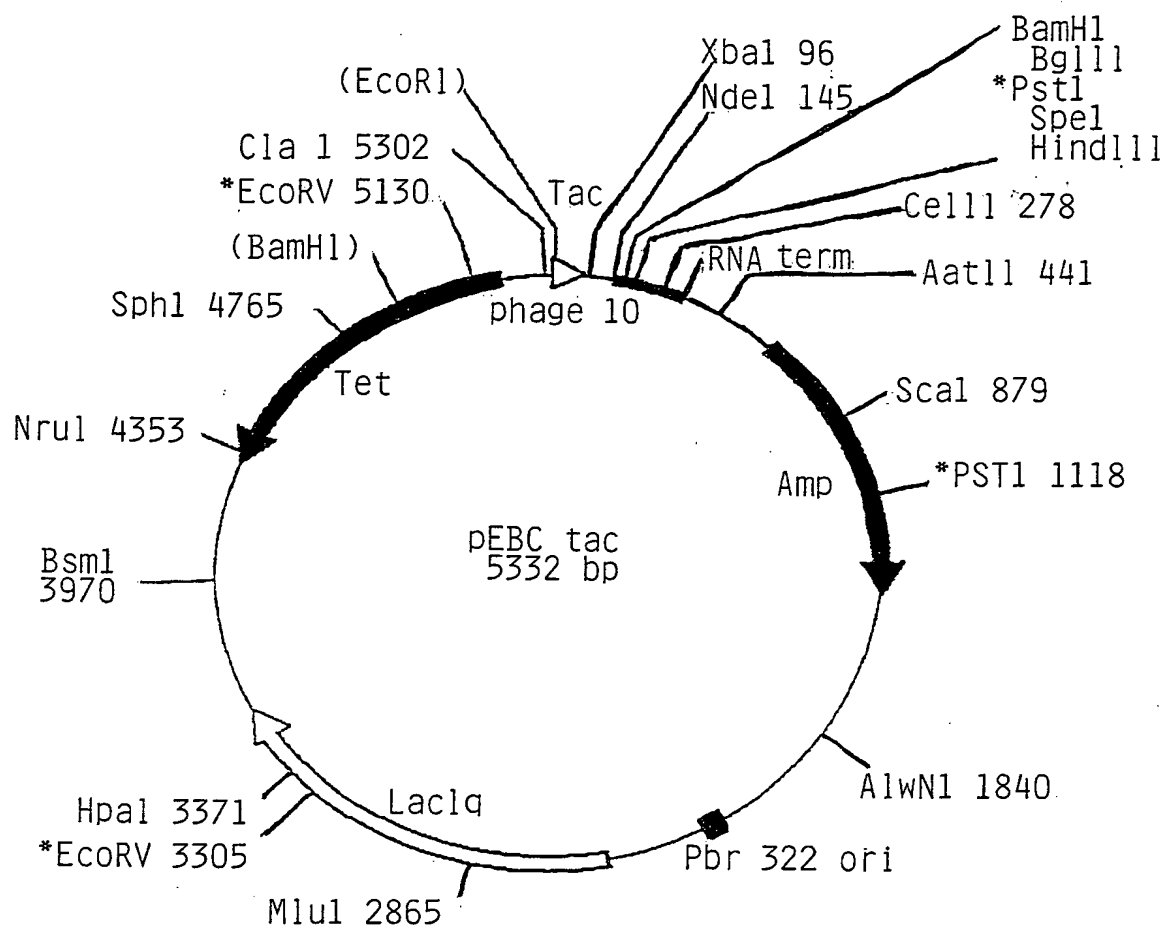


FIG. 11